REMARKS

Reconsideration and withdrawal of the objections and rejections in view of the above amendments and following remarks are respectfully requested. Claims 6, 8, 10, 11, and 12 having been amended, claim 7 having been canceled, claims 22-25 having been added, the pending claims in the above-identified applications are claims 1-6 and 8-25. Of these, claims 6, 8-15, and 22-25 are under examination.

The specification has been amended at page 1, line 36 to complete two WIPO publication numbers. The specification was also amended at page 18, lines 34-35 to disclose the amino acid sequence in a three-letter symbol format with the first letter being capitalized from a one-letter amino symbol format per the Examiner's suggestion.

Claims 6, 8, 10, 11, and 12 have been amended per the Examiner's suggestion. Claims 22-25 have been added. Support for claim 22 can be found, for example, at page 15, lines 11-14. Support for claim 23 can be found, for example, at page 15, lines 15-18. Support for claim 24 and 25 can be found, for example, at page 15, lines 19-31. No new matter has been added.

Priority

The Examiner asserted that the priority document (U.S. Application Serial No. 60/253,924) does not provide adequate support under 35 U.S.C. §119(e) for SEQ ID NO:11 which is recited in claim 11. In order to expedite prosecution of the above-identified patent application, Applicants have deleted claim 11's recitation of SEQ ID NO:7.

Objection to the Specification

The Examiner objected to the specification at page 1, line 36 as being incomplete. Applicants have amended the specification by completing the WIPO publication numbers thereby rendering the objection moot.

The Examiner objected to the specification at page 18, line 34 for not complying with 37 C.F.R. §1.822(d). Applicants have amended the one-letter amino acid sequence to a three-letter amino acid sequence wherein the first letter is capitalized thereby rendering the objection moot.

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Accordingly, withdrawal of the specification objections is respectfully requested.

Rejection Under 35 U.S.C. §101

The Examiner rejected claims 6-15 under 35 U.S.C. §101 as allegedly not being supported by either a specific and substantial credible utility or a well established one. In rejecting the claims, the Examiner stated that "[t]he asserted utility in this case essentially is a method of treating an unspecified, undisclosed disease or condition, which does not define a 'real world' context of use" (page 3 of the Office Action). This rejection is respectfully traversed.

Applicants respectfully submit that the rejection is contrary to both the law and the United States Patent Office's own examination guidelines. The application of these standards to biotechnology inventions is discussed in the January 5, 2001 Federal Register Notice of the United States Patent Office's Utility Examination Guidelines. Section II.B.1(c)(1) and (2) of the January 5, 2001 "Utility Examination Guidelines" states "[a]n invention has a well-established utility if a person of ordinary skill would immediately appreciate why the invention is useful based on the characteristics of the invention (e.g., properties...), and the utility is specific, substantial, and credible." 66 FR 4, p. 1098. Moreover, "[a] patent examiner must accept a utility asserted by an applicant unless the Examiner has sound scientific reasoning to rebut the assertion." 66 FR 4, p. 1096. To establish a *prima facie* showing of lack of utility, "the Office must ... provide a sufficient evidentiary basis for factual assumptions relied upon in establishing the *prima facie* showing ... the PTO must do more than merely question operability - it must set forth factual reasons which would lead one of skill in the art to question the objective truth of the statement of operability." M.P.E.P. §2107.02(IV).

Applicants do not understand this rejection. Applicants maintain, however, that after reading the specification one of skill in the art would immediately appreciate the usefulness of the claimed invention. Applicants would like to draw the Examiner's attention to page 67, lines 1-21, which states, in part:

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> The zacrp13 gene is located at the 22q12.3 region of chromosome 22. Several genes of known function map to this region that are linked to human disease. For example, monosomy of chromosome 22, and less frequently the loss or translocation of distal 22q, is the most common chromosomal abnormality observed in meningioma tumors .... Moreover, the most frequent cytogenetic abnormality in aggressive malignant mesotheliomas is loss of chromosome 22, as well as loss of 22q11.21-q13.1 in acoustic neuromas .... Thus, since the zacrp13 gene maps to chromosome 22q12.3, the zacrp13 polynucleotide probes of the present invention can be used to detect and diagnose the presence of chromosome 22 monosomy and other chromosome 22q12.3 loss, and particularly chromosome 22 monosomy and loss associated with meningiomas, and other human tumors. Moreover, translocation between chromosome 22q12 and chromosome 11q24 (t(11;22)(q24;q12)) is associated with Ewing sarcoma, and other related tumors. Thus, the zacrp13 polynucleotide probes of the present invention can be used to detect and diagnose chromosome 22q12 translocation associated with human disease, such as Ewing sarcoma.

"A diagnostic could assist physicians in determining the type of disease and appropriate therapy, or assistance in genetic counseling" (page 68, lines 9-10 of the specification). Thus, Applicants submit that the ability to detect and diagnosis specific human diseases is a beneficial real world use.

The Examiner has provided no evidence or scientific basis to refute the assertions of utility for the nucleic acid molecules of the present invention. The invention indeed has a specific asserted and a well-established utility for the claimed nucleic acid molecules that are supported by the specification (see above). Thus, Applicants submit that the Examiner has not established a *prima facie* showing of lack of utility, because it has not provided sound scientific reasoning to rebut the assertion of utility in the application and the evidence presented by Applicants therein. In view of the Examiner's apparent failure to note and evaluate this evidence, Applicants submit that a *prima facie* showing of no specific and substantial credible utility has not been made.

For the above reasons, Applicants respectfully submit that the invention recited in claims 6-15 is useful. Accordingly, reconsideration and withdrawal of the rejection under 35 U.S.C. §101 are respectfully requested.

Rejection Under 35 U.S.C. §112, First Paragraph

The Examiner rejected claims 6-15 under 35 U.S.C. §112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention. This rejection is respectfully traversed.

In light of the above remarks with respect to utility, reconsideration and withdrawal of the rejection of claims 6-15 under 35 U.S.C. §112, first paragraph, are respectfully requested.

Rejection Under 35 U.S.C. §112, Second Paragraph

The Examiner rejected claims 6-15 under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. This rejection is respectfully traversed.

The Examiner rejected claim 6 for an indefinite recitation of the term "comprising." Applicants have cosmetically amended claim 6 thereby rendering the rejection moot. Accordingly, withdrawal of the rejection under 35 U.S.C. §112, second paragraph, is respectfully requested.

The Examiner rejected claim 7 as the term "moiety" was unclear. Applicants have canceled claim 7 thereby rendering the rejection moot. Accordingly, withdrawal of the rejection under 35 U.S.C. §112, second paragraph, is respectfully requested.

The Examiner rejected claim 8 as the term "portion" is allegedly unclear. This rejection is respectfully traversed. Applicants do not understand the Examiner's position. Applicants maintain, however, that the term "portion" and the phrases "first portion" and "second portion" are clear to one of skill in the art. The first portion of the fusion protein includes a polypeptide selected from the Markush list, while the second

portion of the fusion protein includes another polypeptide. Applicants submit that one of skill in the art would readily understand the meaning of the term "portion" as recited in claim 8. Accordingly, reconsideration and withdrawal of the rejection of claim 8 under 35 U.S.C. §112, second paragraph, are respectfully requested.

The Examiner rejected claim 9 as the term "collagen-like" is allegedly unclear. The rejection is respectfully traversed. Applicants would like to draw the Examiner's attention to page 19, line 36 through page 20, line 3 which discloses "[a]s used herein the term "collagen" or "collagen-like domain" refers to a series of repeating triplet amino acid sequences, "repeats" or "collagen repeats" represented by the motifs Gly-Xaa-Pro or Gly-Xaa-Xaa, where Xaa is any amino acid reside. The collagen repeats can be continuous or interspersed with triplet gaps." Thus, in view of Applicants' specification, there is clear and sufficient guidance to apprise one of skill in the art of a "collagen-like" domain according to the claimed invention. Accordingly, reconsideration and withdrawal of the rejection of claim 9 under 35 U.S.C. §112, second paragraph, are respectfully requested.

The Examiner rejected claim 10 is being indefinite for reciting an improper Markush group. Applicants have cosmetically amended claim 10 thereby rendering the rejection moot. Accordingly, withdrawal of the rejection under 35 U.S.C. §112, second paragraph, is respectfully requested.

The Examiner rejected claim 11 as being indefinite for reciting overlapping nucleotide ranges. This rejection is respectfully traversed. Applicants are confused by the Examiner's rejection. There is no "broad language . . . followed by 'such as' and then [a] narrow[er] range" or the like (MPEP §706.03(d)). The Markush group is directed towards distinct and precise nucleotide sequences. Thus, Applicants submit that one of skill in the art would clearly understand the boundaries of claim 11. Accordingly, reconsideration and withdrawal of the rejection of claim 11 under 35 U.S.C. §112, second paragraph, are respectfully requested.

The Examiner rejected claim 12 as being indefinite for reciting an improper Markush group. Applicants have cosmetically amended claim 12 thereby rendering the rejection moot. Accordingly, withdrawal of the rejection under 35 U.S.C. §112, second paragraph, is respectfully requested.

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The Examiner rejected claims 13-15 as being indefinite for depending from an indefinite claim (claim 12). This rejection is respectfully traversed. Applicants have amended claim 12 thereby rendering this rejection moot. Accordingly, withdrawal of the rejection of claims 13-15 under 35 U.S.C. §112, second paragraph, is respectfully requested.

Rejection Under 35 U.S.C. §102(a)

The Examiner rejected claims 6-15 under 35 U.S.C. §102(a) as being anticipated by Bridgeman (Accession No. Z82198). Specifically, the Examiner stated that "Bridgeman discloses a human nucleotide sequence that is identical to SEQ ID NO:1 between the base pairs 98 and 1381" (page 6 of the Office Action). This rejection is respectfully traversed.

In order to expedite prosecution of the above-identified patent application, Applicants have amended claim 6 (deleted parts (d) and (e) which are directed towards amino acid residues 60-149 and 46-149 of SEQ ID NO:2, respectively), claim 8 (deleted parts (d) and (e) which are directed towards amino acid residues 60-149 and 46-149 of SEQ ID NO:2, respectively), claim 10 (deleted parts (d) and (e) which are directed towards amino acid residues 60-149 and 46-149 of SEQ ID NO:2, respectively), claim 11 (deleted parts (d) and (e) which are directed towards nucleotides 179-448 and 137-448 of SEQ ID NO:1, respectively), and claim 12 (deleted parts (d) and (e) which are directed towards amino acid residues 60-149 and 46-149 of SEQ ID NO:2, respectively).

Accordingly, withdrawal of the rejection of claims 6-15 under 35 U.S.C. §102(a) is respectfully requested.

Rejection Under 35 U.S.C. §103(a)

The Examiner rejected claims 12-15 under 35 U.S.C. §103 as being unpatentable over Bridgeman (Accession No. Z82198) in view of Lee et al. (Biotechnol. Prog., 15:884-890 (1999)). This rejection is respectfully traversed.

In light of the amendments to claim 12, from which claims 13-15 depend, Applicants submit that this rejection has been rendered moot. Accordingly, withdrawal of the rejection of claims 12-15 under 35 U.S.C. §103(a) is respectfully requested.

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Summary

On the basis of the above amendments and remarks, Applicants believe that each rejection has been addressed and overcome. Reconsideration of the application and its allowance are respectfully requested. If for any reason the Examiner feels that a telephone conference would expedite prosecution of the application, the Examiner is invited to telephone the undersigned at (206) 442-6540.

Respectfully Submitted,

Brian J. Walsh
Registration No. 45,543

Enclosures:

Petition and Fee for Extension of Time (in duplicate)
Information Disclosure Statement
Postcard

APPENDIX A – SPECIFICATION/CLAIM AMENDMENTS WITH NOTATIONS TO INDICATE CHANGES MADE
Applicant(s): Fox et al.
Serial No. 09/997,610
Docket No. 00-96
For: ADIPOCYTE COMPLEMENT RELATED PROTEIN ZACRP13

Amendments to the following are indicated by underlining what has been added and bracketing what has been deleted. Additionally, all amendments have been shaded.

In the Specification

The paragraph beginning at page 1, line 23, has been amended as follows:

The adipocyte complement related protein family plays a role in the interaction of cells with their environment, and appear to act at the interface of the extracellular matrix and the cell. These proteins include, Acrp30 (Scherer et al., *J. Biol. Chem. 270*:26746-49, 1995), apM1 (Maeda et al., *Biochem. Biophys. Res. Comm. 221*:286-9, 1996), GBP28 (Nakano et al., *J. Biochem. 120*:803-12, 1996), zsig39 (Sheppard and Humes, WIPO Published Patent No: WO99/10492), zsig37 (Sheppard, WIPO Published Patent No: WO99/04000), ZCRP30R1 (Smith et al., WIPO Published Patent No. WO99/56619), ACRP30R1L (Hensley et al., WIPO Published Patent No: WO99/59618), ACRP30R2 (Hensley et al., WIPO Published Patent No: WO99/64629), PRO 353 and PRO 344 (Wood et al., WIPO Published Patent No. WO99/28462), zacrp2 (Piddington et al., WO 00/63376), zacrp3 (Piddington et al., WO 00/63377), zacrp4 (Piddington et al., WO 01/02565), zacrp5 (Piddington et al., WO 00/73444), zacrp6 (Piddington et al., WO 00/73466), zacrp11 (Piddington et al., WO [00/****] 02/070704), and zacrp12 (Piddington et al., WO [00/****] 02/44373).

The paragraph beginning at page 18, line 18, has been amended as follows:

The present invention is based in part upon the discovery of a novel DNA sequence that encodes a polypeptide having homology to the adipocyte complement related protein family. The polypeptide has been designated zacrp13. The nucleotide

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sequence of *zacrp13* is described in SEQ ID NO:1, and its deduced amino acid sequence is described in SEQ ID NO:2. The zacrp13 polypeptide includes a signal sequence, comprising amino acid 1 (Ile) to amino acid residue 17 (Val) of SEQ ID NO:2, nucleotides 2-51 of SEQ ID NO:1. The mature polypeptide ranges from amino acid 18 (Ala) to amino acid 459 (Met) of SEQ ID NO:2, nucleotides 52-1378 of SEQ ID NO:1. Within the mature polypeptide is found a collagen-like domain between amino acid 19 (Gly) and 45 (Ile) of SEQ ID NO:2, nucleotides 56-136 of SEQ ID NO:1. In the collagen-like domain there are 5 collagen repeats, three perfect Gly-Xaa-Pro repeats and two imperfect Gly-Xaa-Xaa repeats, and four amino acid triplets interspersed among the collagen repeats. A region from amino acid 46 (Ser) to 59 (Ser) of SEQ ID NO:2, nucleotides 137-178 of SEQ ID NO:1, connects the collagen domain with the C1q domain. The zacrp13 polypeptide also includes a carboxy-terminal C1q domain, ranging from about amino acid 60 (Ala) to 149 (Ala) of SEQ ID NO:2, nucleotides 179-448 of SEQ ID NO:1. An aromatic motif [F]Phe-X(5)-[ND]Asn Asp]-X(4)-[FYWL]Phe Tyr Trp Leu]-X(6)-[F]Phe-X(5)-[G]Gly-X-[Y]Tyr-X(4) (SEQ ID NO:4) is also found within this domain between residues 78 (Phe) and 108 (Phe) of SEQ ID NO:2, nucleotides 233-325 of SEQ ID NO:1. X represents any amino acid residue and the number in parentheses () indicates the amino acid number of residues. The amino acid residues contained within the square parentheses [] restrict the choice of amino acid residues at that particular position. There is a fair amount of conserved structure within the C1q domain to enable proper folding.

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In the Claims

For the Examiner's convenience, all of the pending claims are shown below.

1. An isolated polypeptide selected from the group consisting of:

(a) a polypeptide comprising amino acid residues 19-45 of SEQ ID NO:2;

(b) a polypeptide comprising amino acid residues 18-45 of SEQ ID NO:2;

(c) a polypeptide comprising amino acid residues 1-45 of SEQ ID NO:2;

(d) a polypeptide comprising amino acid residues 60-149 of SEQ ID NO:2;

(e) a polypeptide comprising amino acid residues 46-149 of SEQ ID NO:2;

(f) a polypeptide comprising amino acid residues 19-149 of SEQ ID NO:2;

(g) a polypeptide comprising amino acid residues 18-149 of SEQ ID NO:2;

(h) a polypeptide comprising amino acid residues 1-149 of SEQ ID NO:2; and

(i) a polypeptide comprising amino acid residues 18-459 of SEQ ID NO:2.

2. An isolated polypeptide according to claim 1, wherein said polypeptide further comprises a moiety selected from the group consisting of: affinity tags, toxins, radionucleotides, enzymes, and fluorophores.

3. A fusion protein comprising a first portion and a second portion joined by a peptide bond, said first portion consisting of a polypeptide selected from the group consisting of:

(a) a polypeptide comprising amino acid residues 19-45 of SEQ ID NO:2;

(b) a polypeptide comprising amino acid residues 18-45 of SEQ ID NO:2;

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(c) a polypeptide comprising amino acid residues 1-45 of SEQ ID NO:2;

(d) a polypeptide comprising amino acid residues 60-149 of SEQ ID NO:2;

(e) a polypeptide comprising amino acid residues 46-149 of SEQ ID NO:2;

(f) a polypeptide comprising amino acid residues 19-149 of SEQ ID NO:2;

(g) a polypeptide comprising amino acid residues 18-149 of SEQ ID NO:2;

(h) a polypeptide comprising amino acid residues 1-149 of SEQ ID NO:2; and

(i) a polypeptide comprising amino acid residues 18-459 of SEQ ID NO:2; and

said second portion comprising another polypeptide.

4. A fusion protein according to claim 3, wherein said second portion is a collagen-like domain or a C1Q domain from an adipocyte complement related protein.

5. An isolated polypeptide according to claim 1, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide consisting of amino acid residues 19-45 of SEQ ID NO:2;

(b) a polypeptide consisting of amino acid residues 18-45 of SEQ ID NO:2;

(c) a polypeptide consisting of amino acid residues 1-45 of SEQ ID NO:2;

(d) a polypeptide consisting of amino acid residues 60-149 of SEQ ID NO:2;

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(e) a polypeptide consisting of amino acid residues 46-149 of SEQ ID NO:2;

(f) a polypeptide consisting of amino acid residues 19-149 of SEQ ID NO:2;

(g) a polypeptide consisting of amino acid residues 18-149 of SEQ ID NO:2;

(h) a polypeptide consisting of amino acid residues 1-149 of SEQ ID NO:2; and

(i) a polypeptide consisting of amino acid residues 18-459 of SEQ ID NO:2.

6. (**Amended**) An isolated nucleic acid molecule encoding a polypeptide wherein the encoded polypeptide comprises amino acid residues selected from the group consisting of:

(a) [a polypeptide comprising] amino acid residues 19-45 of SEQ ID NO:2;

(b) [a polypeptide comprising] amino acid residues 18-45 of SEQ ID NO:2;

(c) [a polypeptide comprising] amino acid residues 1-45 of SEQ ID NO:2;

[(d) a polypeptide comprising amino acid residues 60-149 of SEQ ID NO:2;

(e) a polypeptide comprising amino acid residues 46-149 of SEQ ID NO:2;]

([f]d) [a polypeptide comprising] amino acid residues 19-149 of SEQ ID NO:2;

([g]e) [a polypeptide comprising] amino acid residues 18-149 of SEQ ID NO:2;

([h]f) [a polypeptide comprising] amino acid residues 1-149 of SEQ ID NO:2; and

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([i]g) [a polypeptide comprising] amino acid residues 18-459 of SEQ ID NO:2.

7. **(Canceled)** [An isolated nucleic acid molecule encoding a polypeptide according to claim 6, wherein said polypeptide further comprises a moiety selected from the group consisting of: affinity tags, toxins, radionucleotides, enzymes, and fluorophores.]

8. **(Amended)** A nucleic acid molecule encoding a fusion protein comprising a first portion and a second portion joined by a peptide bond, said first portion consisting of a polypeptide selected from the group consisting of:

(a) a polypeptide comprising amino acid residues 19-45 of SEQ ID NO:2;

(b) a polypeptide comprising amino acid residues 18-45 of SEQ ID NO:2;

(c) a polypeptide comprising amino acid residues 1-45 of SEQ ID NO:2;

[(d) a polypeptide comprising amino acid residues 60-149 of SEQ ID NO:2;

(e) a polypeptide comprising amino acid residues 46-149 of SEQ ID NO:2;]

([f]d) a polypeptide comprising amino acid residues 19-149 of SEQ ID NO:2;

([g]e) a polypeptide comprising amino acid residues 18-149 of SEQ ID NO:2;

([h]f) a polypeptide comprising amino acid residues 1-149 of SEQ ID NO:2; and

([i]g) a polypeptide comprising amino acid residues 18-459 of SEQ ID NO:2; and

said second portion comprising another polypeptide.

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9. A nucleic acid molecule encoding a fusion protein according to claim 8, wherein said second portion is a collagen-like domain or a C1Q domain from an adipocyte complement related protein.

10. **(Amended)** An isolated nucleic acid molecule according to claim 6, [wherein the nucleic acid molecule encodes a polypeptide] wherein the encoded polypeptide comprises amino acid residues selected from the group consisting of:

(a) [a polypeptide consisting of] amino acid residues 19-45 of SEQ ID NO:2;

(b) [a polypeptide consisting of] amino acid residues 18-45 of SEQ ID NO:2;

(c) [a polypeptide consisting of] amino acid residues 1-45 of SEQ ID NO:2;

[(d) a polypeptide consisting of amino acid residues 60-149 of SEQ ID NO:2;

(e) a polypeptide consisting of amino acid residues 46-149 of SEQ ID NO:2;]

([f]d) [a polypeptide consisting of] amino acid residues 19-149 of SEQ ID NO:2;

([g]e) [a polypeptide consisting of] amino acid residues 18-149 of SEQ ID NO:2;

([h]f) [a polypeptide consisting of] amino acid residues 1-149 of SEQ ID NO:2; and

([i]g) [a polypeptide consisting of] amino acid residues 18-459 of SEQ ID NO:2.

11. **(Amended)** An isolated nucleic acid molecule selected from the group consisting of:

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(a) a nucleic acid molecule consisting of nucleotides 56-136 of SEQ ID NO:1;

(b) a nucleic acid molecule consisting of nucleotides 53-156 of SEQ ID NO:1;

(c) a nucleic acid molecule consisting of nucleotides 2-156 of SEQ ID NO:1;

[(d) a nucleic acid molecule consisting of nucleotides 179-448 of SEQ ID NO:1;

(e) a nucleic acid molecule consisting of nucleotides 137-448 of SEQ ID NO:1;]

([f]d) a nucleic acid molecule consisting of nucleotides 56-448 of SEQ ID NO:1;

([g]e) a nucleic acid molecule consisting of nucleotides 53-448 of SEQ ID NO:1;

([h]f) a nucleic acid molecule consisting of nucleotides 2-448 of SEQ ID NO:1;

([i]g) a nucleotide molecule consisting of nucleotides 2-1378 of SEQ ID NO:1; and

([j]h) a nucleic acid molecule consisting of SEQ ID NO:3[or SEQ ID NO:7].

12. **(Amended)** An expression vector comprising the following operably linked elements:

a transcription promoter;

a DNA segment encoding a polypeptide wherein the encoded polypeptide comprises amino acid residues [with an amino acid sequence] selected from the group consisting of:

(a) amino acid residues 19-45 of SEQ ID NO:2;

(b) amino acid residues 18-45 of SEQ ID NO:2;

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(c) amino acid residues 1-45 of SEQ ID NO:2;

(d) amino acid residues 60-149 of SEQ ID NO:2;

(e) amino acid residues 46-149 of SEQ ID NO:2;

([f]d) amino acid residues 19-149 of SEQ ID NO:2;

([g]e) amino acid residues 18-149 of SEQ ID NO:2;

([h]f) amino acid residues 1-149 of SEQ ID NO:2 and

([i]g) a polypeptide consisting of amino acid residues 18-459 of SEQ ID NO:2; and

a transcription terminator.

13. An expression vector according to claim 12, further comprising a secretory signal sequence operably linked to the DNA segment.

14. A cultured cell into which has been introduced an expression vector according to claim 12, wherein the cell expresses a polypeptide encoded by said DNA segment.

15. A method of producing a polypeptide comprising:

culturing a cell according to claim 14; and isolating the polypeptide produced by the cell.

16. A method of producing an antibody to a polypeptide comprising:

inoculating an animal with a polypeptide selected from the group consisting of:

(a) a polypeptide consisting of 9 to 252 amino acids, wherein the polypeptide is a contiguous sequence of amino acids in SEQ ID NO:2 from amino acid residue 1 to amino acid residue 459;

(b) a polypeptide consisting of amino acid residues 19-45 of SEQ ID NO:2;

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(c) a polypeptide consisting of amino acid residues 18-45 of SEQ ID NO:2;

(d) a polypeptide consisting of amino acid residues 1-45 of SEQ ID NO:2;

(e) a polypeptide consisting of amino acid residues 60-149 of SEQ ID NO:2;

(f) a polypeptide consisting of amino acid residues 56-149 of SEQ ID NO:2;

(g) a polypeptide consisting of amino acid residues 19-149 of SEQ ID NO:2;

(h) a polypeptide consisting of amino acid residues 18-149 of SEQ ID NO:2;

(i) a polypeptide consisting of amino acid residues 1-149 of SEQ ID NO:2; and

(j) a polypeptide consisting of amino acid residues 18-459 of SEQ ID NO:2; and

wherein the polypeptide elicits an immune response in the animal to produce the antibody; and

isolating the antibody from the animal.

17. An antibody produced by the method of claim 16, which binds to a polypeptide of SEQ ID NO:2.

18. An antibody according to claim 17, wherein said antibody is selected from the group consisting of:

(a) polyclonal antibody;

(b) murine monoclonal antibody;

(c) humanized antibody derived from b);

(d) an antibody fragment; and

(e) human monoclonal antibody.

19. An antibody fragment according to claim 18, wherein said antibody fragment is selected from the group consisting of F(ab'), F(ab), Fab', Fab, Fv, scFv, and minimal recognition unit.

20. An anti-idiotype antibody that specifically binds to said antibody of claim 17.

21. An antibody that specifically binds to a polypeptide of claim 1.

22. (New) The isolated nucleic acid molecule of claim 6 wherein the polypeptide further comprises a therapeutic agent.

23. (New) The isolated nucleic acid molecule of claim 6 wherein the polypeptide further comprises a detectable label.

24. (New) The isolated nucleic acid molecule of claim 6 wherein the polypeptide further comprises an affinity tag.

25. (New) The isolated nucleic acid molecule of claim 6 wherein the polypeptide further comprises an enzyme.

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